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Comparative functional genomic study of substrate specificity evolution of the SABATH family of methyltransferases in plants

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Background

The plant SABATH protein family is composed of a group of related small molecule methyltransferases (MTs) that catalyze the S-adenosyl-L-methionine dependent methylation of a variety of plant small molecular weight metabolites encompassing widely divergent structures. Some of these substrates are important plant hormones and signaling molecules, such as indole-3-acetic acid (IAA), jasmonic acid (JA) and salicylic acid (SA). Methylating these compounds may have important impacts on plant growth and development. In the previous paper, we presented Indole-3-acetic acid (IAA) methyltransferase (IAMT) as an evolutionarily ancient member of the SABATH family in higher plants. Whether the IAMT exists in less evolutionarily advanced plants is still unknown.

Materials and methods

To further understand the evolution of the SABATH family in land plants, we undertook an integrated functional genomic approach to identify and characterize *SABATH* genes in a lower plant moss (*Physcomitrella patens*). Four putative moss SABATH genes were identified using bioinformatics tools.

Results and conclusion

Enzymatic assay displayed none of them had IAMT activity, suggesting that IAMT might be evolved after the divergence of lower and higher plants. However, one of them, *PpSABATH1,* showed methyltransferase activity with a number of compounds containing sulhydryl or selenohydryl groups. Tobacco plants overexpressing the *PpSABATH1* gene under the control of CaMV35S promoter exhibited an enhanced tolerance to thiobenzoic acid. Together with these results, we hypothesize that IAMT, the evolutionarily ancient member of the SABATH family in higher plants, evolved from a sulfur methyltransferase.

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